

SEQUENCE LISTING

<110> Nakamura, Yusuke
 Katagiri, Toyomasa
 Nakatsuru, Shuichi

<120> METHOD OF DIAGNOSING BREAST CANCER

<130> 082368-007400US

<150> PCT/JP2004/011741

<151> 2004-08-10

<150> US 60/505,571

<151> 2003-09-24

<160> 34

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 928

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)...(720)

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 ggggatc atg cag aga gct tca cgt ctg aag aga gag ctg cac atg tta 168
 Met Gln Arg Ala Ser Arg Leu Lys Arg Glu Leu His Met Leu
 1 5 10

gcc aca gag cca ccc cca ggc atc aca tgt tgg caa gat aaa gac caa 216
 Ala Thr Glu Pro Pro Pro Gly Ile Thr Cys Trp Gln Asp Lys Asp Gln
 15 20 25 30

atg gat gac ctg cga gct caa ata tta ggt gga gcc aac aca cct tat 264
 Met Asp Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr
 35 40 45

gag aaa ggt gtt ttt aag cta gaa gtt atc att cct gag agg tac cca 312
 Glu Lys Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro
 50 55 60

ttt gaa cct cct cag atc cga ttt ctc act cca att tat cat cca aac 360
 Phe Glu Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn
 65 70 75

att gat tct gct gga agg att tgt ctg gat gtt ctc aaa ttg cca cca 408
 Ile Asp Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro
 80 85 90

aaa ggt gct tgg aga cca tcc ctc aac atc gca act gtg ttg acc tct 456
 Lys Gly Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser
 95 100 105 110

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att cag ctg ctc atg tca gaa ccc aac cct gat gac ccg ctc atg gct 504
Ile Gln Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala
115 120 125

gac ata tcc tca gaa ttt aaa tat aat aag cca gcc ttc ctc aag aat 552
Asp Ile Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn
130 135 140

gcc aga cag tgg aca gag aag cat gca aga cag aaa caa aag gct gat 600
Ala Arg Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp
145 150 155

gag gaa gag atg ctt gat aat cta cca gag gct ggt gac tcc aga gta 648
Glu Glu Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val
160 165 170

cac aac tca aca cag aaa agg aag gcc agt cag cta gta ggc ata gaa 696
His Asn Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu
175 180 185 190

aag aaa ttt cat cct gat gtt tag gggacttgct ctggttcacg ttagttaatg 750
Lys Lys Phe His Pro Asp Val *
195

tggtctttgc caaggtgatc taagttgcct accttgaatt tttttttaaa tatatttgat 810
gacataatgt ttgtgtagtt tatttatctt gtacatatgt attttgaaat cttttaaac 870
tgaaaaataa atagtcattt aatgttgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 928

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<212> PRT
<213> Homo sapiens

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20 25 30
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35 40 45
Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro Phe Glu
50 55 60
Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn Ile Asp
65 70 75 80
Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro Lys Gly
85 90 95
Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser Ile Gln
100 105 110
Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala Asp Ile
115 120 125
Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn Ala Arg
130 135 140
Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp Glu Glu
145 150 155 160
Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val His Asn
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Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu Lys Lys
180 185 190
Phe His Pro Asp Val
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 <222> (53)...(1189)

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 Gly Ala Gly Val Ala Ala Gly Thr Arg Pro Pro Ser Ser Pro Thr Pro
5 10 15

ggc tct cgg cgc cgg cgc cag cgc ccc tct gtg ggc gtc cag tcc ttg 154
 Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln Ser Leu
20 25 30

agg ccg cag agc ccg cag ctc agg cag agc gac ccg cag aaa cgg aac 202
 Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys Arg Asn
35 40 45 50

ctg gac ctg gag aaa agc ctg cag ttc ctg cag cag cag cac tcg gag 250
 Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His Ser Glu
55 60 65

atg ctg gcc aag ctc cat gag gag atc gag cat ctg aag cgg gaa aac 298
 Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg Glu Asn
70 75 80

aag gat ctc cat tac aag ctc ata atg aat cag aca tca cag aag aaa 346
 Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln Lys Lys
85 90 95

gat ggc ccc tca gga aac cac ctt tcc agg gcc tct gct ccc ttg ggc 394
 Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro Leu Gly
100 105 110

gct cgc tgg gtc tgc atc aac gga gtg tgg gta gag ccg gga gga ccc 442
 Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly Gly Pro
115 120 125 130

agc cct gcc agg ctg aag gag ggc tcc tca cgg aca cac agg cca gga 490
 Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg Pro Gly
135 140 145

ggc aag cgt ggg cgt ctt gcg ggc ggt agc gcc gac act gtg cgc tct 538
 Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val Arg Ser
150 155 160

cct gca gac agc ctc tcc atg tca agc ttc cag tct gtc aag tcc atc 586
 Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys Ser Ile
165 170 175

tct aat tca ggc aag gcc agg ccc cag ccc ggc tcc ttc aac aag caa 634

Ser	Asn	Ser	Gly	Lys	Ala	Arg	Pro	Gln	Pro	Gly	Ser	Phe	Asn	Lys	Gln	
180						185					190					
gat	tca	aaa	gct	gac	gtc	tcc	cag	aag	gcg	gac	ctg	gaa	gag	gag	ccc	682
Asp	Ser	Lys	Ala	Asp	Val	Ser	Gln	Lys	Ala	Asp	Leu	Glu	Glu	Glu	Pro	
195					200					205					210	
cta	ctt	cac	aac	agc	aag	ctg	gac	aaa	gtt	cct	ggg	gta	caa	ggg	cag	730
Leu	Leu	His	Asn	Ser	Lys	Leu	Asp	Lys	Val	Pro	Gly	Val	Gln	Gly	Gln	
				215					220					225		
gcc	aga	aag	gag	aaa	gca	gag	gcc	tct	aat	gca	gga	gct	gcc	tgt	atg	778
Ala	Arg	Lys	Glu	Lys	Ala	Glu	Ala	Ser	Asn	Ala	Gly	Ala	Ala	Cys	Met	
			230					235					240			
ggg	aac	agc	cag	cac	cag	ggc	agg	cag	atg	ggg	gcg	ggg	gca	cac	ccc	826
Gly	Asn	Ser	Gln	His	Gln	Gly	Arg	Gln	Met	Gly	Ala	Gly	Ala	His	Pro	
		245					250					255				
cca	atg	atc	ctg	ccc	ctt	ccc	ctg	cga	aag	ccc	acc	aca	ctt	agg	cag	874
Pro	Met	Ile	Leu	Pro	Leu	Pro	Leu	Arg	Lys	Pro	Thr	Thr	Leu	Arg	Gln	
	260					265					270					
tgc	gaa	gtg	ctc	atc	cgc	gag	ctg	tgg	aat	acc	aac	ctc	ctg	cag	acc	922
Cys	Glu	Val	Leu	Ile	Arg	Glu	Leu	Trp	Asn	Thr	Asn	Leu	Leu	Gln	Thr	
275					280					285					290	
caa	gag	ctg	cgg	cac	ctc	aag	tcc	ctc	ctg	gaa	ggg	agc	cag	agg	ccc	970
Gln	Glu	Leu	Arg	His	Leu	Lys	Ser	Leu	Leu	Glu	Gly	Ser	Gln	Arg	Pro	
				295				300						305		
cag	gca	gcc	ccg	gag	gaa	gct	agc	ttt	ccc	agg	gac	caa	gaa	gcc	acg	1018
Gln	Ala	Ala	Pro	Glu	Glu	Ala	Ser	Phe	Pro	Arg	Asp	Gln	Glu	Ala	Thr	
			310					315					320			
cat	ttc	ccc	aag	gtc	tcc	acc	aag	agc	ctc	tcc	aag	aaa	tgc	ctg	agc	1066
His	Phe	Pro	Lys	Val	Ser	Thr	Lys	Ser	Leu	Ser	Lys	Lys	Cys	Leu	Ser	
		325					330					335				
cca	cct	gtg	gcg	gag	cgt	gcc	atc	ctg	ccc	gca	ctg	aag	cag	acc	ccg	1114
Pro	Pro	Val	Ala	Glu	Arg	Ala	Ile	Leu	Pro	Ala	Leu	Lys	Gln	Thr	Pro	
		340				345					350					
aag	aac	aac	ttt	gcc	gag	agg	cag	aag	agg	ctg	cag	gca	atg	cag	aaa	1162
Lys	Asn	Asn	Phe	Ala	Glu	Arg	Gln	Lys	Arg	Leu	Gln	Ala	Met	Gln	Lys	
355				360					365					370		
cgg	cgc	ctg	cat	cgc	tca	gtg	ctt	tga	gccaccccaa	tctgggtcagt						1209
Arg	Arg	Leu	His	Arg	Ser	Val	Leu	*								
				375												
gccaggccca	ccaacctgca	gctggagact	ggctctctat	agcatttcct	gatacttccg											1269
ctacttttag	gcctggctaa	attccaagac	agataacact	caagatagat	aaagtacttg											1329
atctccaaac	tgacaaactg	tttatcttct	agctgttatt	ttgctatttg	gcatttacat											1389
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<210> 4

<211> 378

<212> PRT

<213> Homo sapiens

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 20      25      30
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 35      40      45
Arg Asn Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His
 50      55      60
Ser Glu Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg
 65      70      75      80
Glu Asn Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln
 85      90      95
Lys Lys Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro
 100     105     110
Leu Gly Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly
 115     120     125
Gly Pro Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg
 130     135     140
Pro Gly Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val
 145     150     155     160
Arg Ser Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys
 165     170     175
Ser Ile Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn
 180     185     190
Lys Gln Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu
 195     200     205
Glu Pro Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln
 210     215     220
Gly Gln Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala
 225     230     235     240
Cys Met Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala
 245     250     255
His Pro Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu
 260     265     270
Arg Gln Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu
 275     280     285
Gln Thr Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln
 290     295     300
Arg Pro Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu
 305     310     315     320
Ala Thr His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys
 325     330     335
Leu Ser Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln
 340     345     350
Thr Pro Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met
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cccgcctccc ctccgcgtga gctctgggat ggtccgcgcc gggagcgcgc gcgaggcttg 180
aagcgcgggt gaagcgcgca ggtcggagtg acagctgcgc tgccggcccg gctgcggtca 240
gcaacgcgcc atg gac gca gag ctg gca gag gtg cgc gcc ttg caa gct 289
      Met Asp Ala Glu Leu Ala Glu Val Arg Ala Leu Gln Ala
            1             5             10

gag atc gcg gcc ctg cgg cga gcg tgt gag gac cca ccg gcg ccc tgg 337
Glu Ile Ala Ala Leu Arg Arg Ala Cys Glu Asp Pro Pro Ala Pro Trp
      15             20             25

gaa gag aag tcc cga gtc caa aaa tct ttt caa gcc ata cac caa ttc 385
Glu Glu Lys Ser Arg Val Gln Lys Ser Phe Gln Ala Ile His Gln Phe
      30             35             40             45

aat ttg gaa gga tgg aag tct tca aaa gat ctg aaa aat cag ctt gga 433
Asn Leu Glu Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly
            50             55             60

cat tta gaa tca gaa ctt tca ttt cta agt acg ctt act ggc atc aat 481
His Leu Glu Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn
            65             70             75

ata aga aat cac tcc aag cag aca gaa gac cta aca agc act gag atg 529
Ile Arg Asn His Ser Lys Gln Thr Glu Asp Leu Thr Ser Thr Glu Met
            80             85             90

aca gaa aag agt att aga aaa gtt cta cag aga cac aga tta tca gga 577
Thr Glu Lys Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly
            95             100             105

aat tgc cac atg gtt aca ttt caa ctt gaa ttt cag att ctg gaa att 625
Asn Cys His Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile
      110             115             120             125

cag aat aag gag aga tta tct tct gct gtt act gac ctc aac ata ata 673
Gln Asn Lys Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile
            130             135             140

atg gag ccc aca gaa tgc tca gaa tta agt gaa ttt gtg tct aga gca 721
Met Glu Pro Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala
            145             150             155

gaa gag aga aaa gat ctg ttc atg ttt ttc cga agc ctg cat ttt ttt 769
Glu Glu Arg Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe
            160             165             170

gtg gag tgg ttt gaa tat cgt aag cgc acg ttt aaa cat ctc aag gaa 817
Val Glu Trp Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu
            175             180             185

aag tac cca gat gcc gtg tac ctc tcg gag ggg ccc tcc tcc tgc tcc 865
Lys Tyr Pro Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser
      190             195             200             205

atg ggg atc cgc agc gcc agc cgg cca ggg ttt gaa tta gtc att gtt 913
Met Gly Ile Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val
            210             215             220

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tgg agg ata caa ata gat gaa gat ggg aag gtt ttt cca aag ctg gat 961
 Trp Arg Ile Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp
 225 230 235

 ctt ctc acc aaa gtc cca cag cga gcc ctg gag ctg gac aag aac aga 1009
 Leu Leu Thr Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg
 240 245 250

 gcc ata gaa act gct cct ctc agc ttc cga acc ctg gta gga ctg ctt 1057
 Ala Ile Glu Thr Ala Pro Leu Ser Phe Arg Thr Leu Val Gly Leu Leu
 255 260 265

 gga atc gaa gct gct ctg gaa agc ctg ata aaa tcg ctt tgt gca gag 1105
 Gly Ile Glu Ala Ala Leu Glu Ser Leu Ile Lys Ser Leu Cys Ala Glu
 270 275 280 285

 gag aac aac tagttccaaa acagtgaacg tggaggatga agatgctgcg 1154
 Glu Asn Asn

tggaggaaca tgcaatttta ttcaatataa acatttgcta ttttctgctt agaaaccaca 1214
 ccctgaagac gtgctgtcta tgcagttatg gcacattata tggaaactct catgacatga 1274
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 35 40 45
 Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly His Leu Glu
 50 55 60
 Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn Ile Arg Asn
 65 70 75 80
 His Ser Lys Gln Thr Glu Asp Leu Thr Ser Thr Glu Met Thr Glu Lys
 85 90 95
 Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly Asn Cys His
 100 105 110
 Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile Gln Asn Lys
 115 120 125
 Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile Met Glu Pro
 130 135 140
 Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala Glu Glu Arg
 145 150 155 160
 Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe Val Glu Trp
 165 170 175
 Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu Lys Tyr Pro
 180 185 190
 Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser Met Gly Ile
 195 200 205
 Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val Trp Arg Ile
 210 215 220
 Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp Leu Leu Thr
 225 230 235 240
 Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg Ala Ile Glu

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Thr	Ala	Pro	Leu	Ser	Phe	Arg	Thr	Leu	Val	Gly	Leu	Leu	Gly	Ile	Glu				
			260					265					270						
Ala	Ala	Leu	Glu	Ser	Leu	Ile	Lys	Ser	Leu	Cys	Ala	Glu	Glu	Asn	Asn				
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<210> 8
 <211> 23
 <212> DNA
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<220>
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<400> 8
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<210> 9
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<400> 9
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<210> 10
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<400> 10
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<210> 11
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<220>
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RT-PCR

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<210> 14
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RT-PCR

<400> 14
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<210> 15
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<220>
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RT-PCR

<400> 15
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<210> 16
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RT-PCR

<400> 16
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<210> 17
<211> 30
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<210> 18
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<220>
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<400> 18
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<210> 19
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<220>
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<400> 20
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<210> 21
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<210> 22
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 <210> 23
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 <210> 25
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 <220>
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 <210> 26
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 <212> DNA
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 <400> 26
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 <210> 27
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<220>
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 <400> 27
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 <210> 28
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 <220>
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 <400> 28
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 <210> 29
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 <220>
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